Supporting Online Material for

The Piwi/piRNA Pathway Provides an Adaptive Defense in the Transposon Arms Race

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Supporting Online Material

Table S1. Argonaute proteins and associated small RNA in *Drosophila* and mouse

	AGO clade		**PIWI clade**	
	mouse	*Drosophila*	mouse	*Drosophila*
Members	AGO1-4	AGO1, AGO2	MILI, MIWI, MIWI2	Piwi, Aubergine, AGO3
Expression	ubiquitous	ubiquitous	germline (predominantly testes)	female and male germline
Small RNA partners, size	*miRNAs* and exogenous *siRNAs* 21-23nt	*miRNAs* (preferentially AGO1) viral *siRNAs* (AGO2) 21-23nt	*piRNAs* 26-30nt	*piRNAs* (former *rasiRNAs*) 24-28nt
Slicer activity	AGO2	AGO1, AGO2	unknown	Piwi, Aub, AGO3
Small RNA biogenesis	*miRNAs*: Drosha, Dicer	miRNAs: Drosha, Dicer-1 siRNAs: Dicer-2	primary *piRNA*: unknown secondary *piRNA*: Slicer activity of Piwis and unknown 3' processing factor	
Function	*miRNAs*: translational repression and degradation of endogenous mRNAs exogenous *siRNAs*: RNAi	*miRNAs*: translational repression and degradation of endogenous mRNAs viral *siRNAs*: inhibition of viral replication	transposon silencing; guiding DNA-methylation to repeats?	transposon silencing; regulation of heterochromatin?

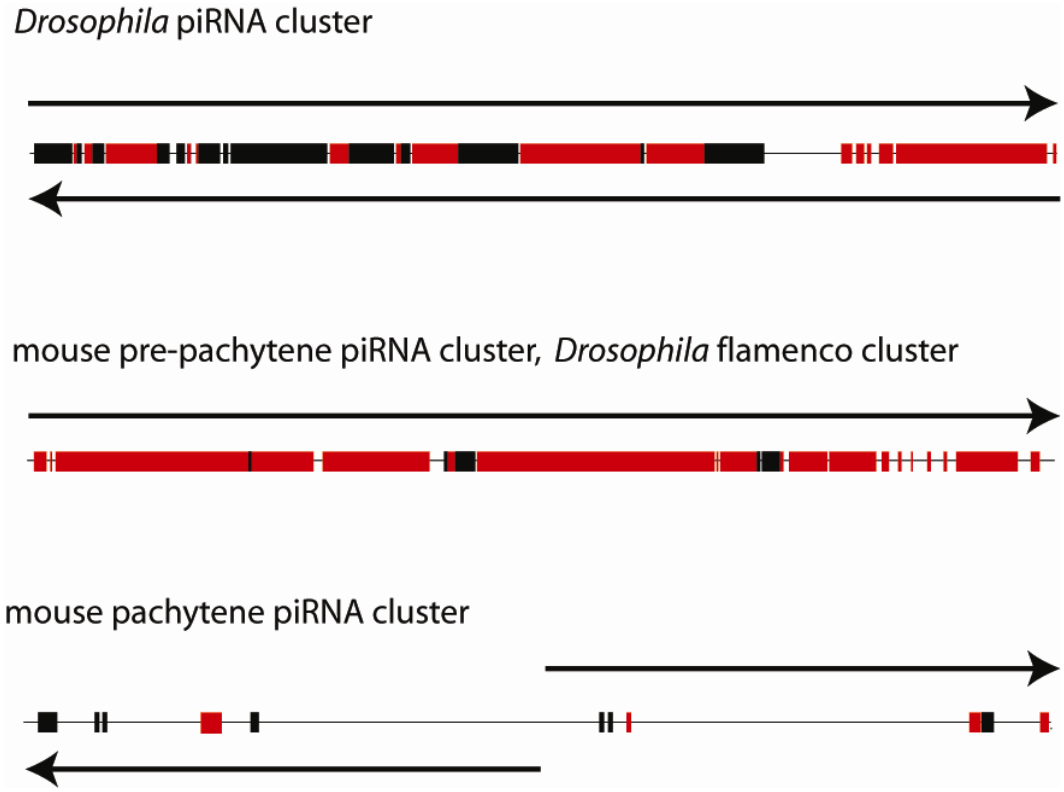

Figure S1. Different piRNA cluster types in *Drosophila* and mouse.
Solid bars indicate transposons (black in sense orientation, red in antisense). Arrows indicate the strand from which piRNAs are derived. In typical *Drosophila* clusters piRNAs originate from both genomic strands. In mammalian pre-pachytene clusters and few *Drosophila* clusters (e.g. flamenco) piRNAs originate exclusively from one genomic strand. In this case, orientation of majority of transposons is antisense to piRNA transcription. Pachytene piRNA clusters have low transposon content and often bidirectional.